



#10/a

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: BOIME, Irving
MOYLE, William R.
- (ii) TITLE OF THE INVENTION: SINGLE-CHAIN FORMS OF THE GLYCOPROTEIN HORMONE QUARTET
- (iii) NUMBER OF SEQUENCES: 83

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 2000 Pennsylvania Avenue, NW, suite 5500
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20006-1888

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/918,288
(B) FILING DATE: 25 AUG-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/853,524
(B) FILING DATE: 09-MAY-1997
- (A) APPLICATION NUMBER: 08/199,382
(B) FILING DATE: 18-FEB-1994

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Murashige, Kate H
(B) REGISTRATION NUMBER: 29,959
(C) REFERENCE/DOCKET NUMBER: 29500-20050.25

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 202-887-1500
(B) TELEFAX: 202-887-0763
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg
1 5 10 15
Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
20 25

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 836 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 33...827
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGAAATCGA CGGAATCAGA CTCGAGCAA GG ATG GAG ATG TTC CAG GGG CTG Met Glu Met Phe Gln Gly Leu	53
1 5	
CTG CTG TTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu	101
10 15 20	
CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu	149
25 30 35	
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala	197
40 45 50 55	
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala	245
60 65 70	
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile	293
75 80 85	
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala	341
90 95 100	
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp	389

105	110	115	
TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe 120 125 130 135			437
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC AGC CTT CCA AGC CCA Gln Asp Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro 140 145 150			485
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser 155 160 165			533
GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA TGC Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys 170 175 180			581
ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA CTT Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu 185 190 195			629
CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA AGG Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg 200 205 210 215			677
TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC ACT Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr 220 225 230			725
TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT TTC Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe 235 240 245			773
AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT CAC Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His 250 255 260			821
AAA TCT TAAGGTACC Lys Ser 265			836

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Ser Met Gly

1	5	10	15
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile			
20	25	30	
Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr			
35	40	45	
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val			
50	55	60	
Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg			
65	70	75	80
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val			
85	90	95	
Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu			
100	105	110	
Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu			
115	120	125	
Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Lys Ala Pro			
130	135	140	
Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr			
145	150	155	160
Pro Ile Leu Pro Gln Gly Ser Gly Ser Gly Ser Ala Pro Asp			
165	170	175	
Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser			
180	185	190	
Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg			
195	200	205	
Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys			
210	215	220	
Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg			
225	230	235	240
Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His			
245	250	255	
Cys Ser Thr Cys Tyr Tyr His Lys Ser			
260	265		

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGGATTAG CTTGAGATGG ATCCGGTACC TTAAGATTTG TGATAATAAC AAGTACTGCA	60
GTGGCACGCC GTGTGGTTCT CCACCTTGAA ACCCCCCATT ACTGTGACCC TGTATATGA	120
TTTAGCTACA CAGCAAGTGG ACTCTGAGGT GACGTTCTT TGGACCAACA TCGTCTTCTT	180
GGACCTTAGT GGAGTGGGAT ATGCTCTAGA GAAGCAGCAG CCCATGCACT GAAGTATTGG	240
GGCACCCGGC TGGGAGAAGA ATGGGTTTTC CTGTAGCGTG CATTCTGGGC AATCCTGCAC	300
ATCAGGAGCG CTACCAAGATC CGCTACCGGA TCCTTGGGG AGGATCGGGG TGTCCGAGGG	360
CCCCGGGAGT CGGGATGGGC TTGGAAGGCT GGGGGGAGGG GCCTTGAGG AAGAGGAGTC	420
CTGGAAGCGG GGGTCATCAC AGGTCAAGGG GTGGTCCTTG GGACCCCCGC AGTCAGTGGT	480
GCTGCGGCGG CAGAGTGCAC ATTGACAGCT GAGAGCCACG GCGTAGGAGA CCACGGGTT	540
CACGCCGCGC GGGCAGGCCAG GGAGCCGGAT GGACTCGAAG CGCACATCGC GGTAGTTGCA	600
CACCACCTGA GGCAGGGCCG GCAGGACCCC CTGCAGCACG CGGGTCATGG TGGGGCAGTA	660
GCCGGCACAG ATGGTGGTGT TGACGGTGAT GCACACGGGG CAGCCCTCCT TCTCCACAGC	720

CAGGGTGGCA TTGATGGGGC GGCACCGTGG CCGAAGCGGC TCCTTGGATG CCCATGTCCC 780
 GCCCATGCTC AGCAGCAGCA ACAGCAGCAG CCCCTGGAAC ATCTCCATCC TTGG 834

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 33...734
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG GAG ATG TTC CAG GGG CTG 53
Met Glu Met Phe Gln Gly Leu
1 5

CTG CTG TTG CTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG 101
 Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu
 10 15 20

CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG 149
 Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu
 25 30 35

AAG	GAG	GGC	TGC	CCC	GTG	TGC	ATC	ACC	GTC	AAC	ACC	ACC	ATC	TGT	GCC	197
Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr	Ile	Cys	Ala	
40					45					50					55	

GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC 245
 Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala
 60 65 70

CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC 293
 Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile
 75 80 85

CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC 341
 Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala
 90 95 100

GTC GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC 389
 Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp
 105 110 115

TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCG CGG GGA 437
 Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Gly
 120 125 130 135

TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA 485
 Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu

130	135	140
Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe		
145	150	155
Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser		
165	170	175
Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln		
180	185	190
Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn		
195	200	205
Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys		
210	215	220
His Cys Ser Thr Cys Tyr Tyr His Lys Ser		
225	230	

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTACCTTAA GATTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC	60
TTGAAACCC CCCATTACTG TGACCCCTGTT ATATGATTAA GCTACACAGC AAGTGGACTC	120
TGAGGTGACG TTCTTTGGA CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC	180
TCTAGAGAAC CAGCAGCCCCA TGCAGTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG	240
GTTCACGCTGT AGCGTGCATT CTGGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT	300
ACCGGATCCC CGCGGGTCAT CACAGGTCAA GGGGTGGTCC TTGGGACCCC CGCAGTCAGT	360
GGTGCTGCGG CGGCAGAGTG CACATTGACA GCTGAGAGCC ACGGCGTAGG AGACCACGGG	420
GTTCACGCGG CGCGGGCAGC CAGGGAGCCG GATGGACTCG AAGCGCACAT CGCGGTAGTT	480
GCACACCACC TGAGGGCAGGG CGGGCAGGAC CCCCTGCAGC ACGCGGGTCA TGGTGGGGCA	540
GTAGCCGGCA CAGATGGTGG TGTTGACGGT GATGCACACG GGGCAGCCCT CCTCTCCAC	600
AGCCAGGGTG GCATTGATGG GGCAGGCACCG TGGCCGAAGC GGCTCCTTGG ATGCCCATGT	660
CCCGCCCCATG CTCAGCAGCA GCAACAGCAG CAGCCCCTGG AACATCTCCA TCCTTGG	717

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 34...735
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GGA ATG GAG ATG CTC CAG GGG CTG	54
Met Glu Met Leu Gln Gly Leu	
1	5

140	145	150	
TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile 155	160	165	533
CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu 170	175	180	581
AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser 185	190	195	629
ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTC ATG GGG GGT Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly 200	205	210	677
TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr 220	225	230	725
CAC AAA TCT TAAGGTACC His Lys Ser			743

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly 1	5	10	15
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile 20	25	30	
Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr 35	40	45	
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val 50	55	60	
Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg 65	70	75	80
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val 85	90	95	
Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu 100	105	110	
Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu 115	120	125	
Thr Cys Asp Asp Pro Arg Gly Ser Gly Ser Gly Ser Ala Pro			

CTG CTG TTG CTG CTG AGC ATG GGC GGG GCA TGG GCA TCC AGG GAG	102
Leu Leu Leu Leu Leu Ser Met Gly Gly Ala Trp Ala Ser Arg Glu	
10 15 20	
CCG CTT CGG CCA TGG TGC CAC CCC ATC AAT GCC ATC CTG GCT GTG GAG	150
Pro Leu Arg Pro Trp Cys His Pro Ile Asn Ala Ile Leu Ala Val Glu	
25 30 35	
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC	198
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala	
40 45 50 55	
GGC TAC TGC CCC ACC ATG ATG CGC GTG CTG CAG GCG GTC CTG CCG CCC	246
Gly Tyr Cys Pro Thr Met Met Arg Val Leu Gln Ala Val Leu Pro Pro	
60 65 70	
CTG CCT CAG GTG GTG TGC ACC TAC CGT GAT GTG CGC TTC GAG TCC ATC	294
Leu Pro Gln Val Val Cys Thr Tyr Arg Asp Val Arg Phe Glu Ser Ile	
75 80 85	
CGG CTC CCT GGC TGC CCG CGT GGC GTG GAC CCC GTG GTC TCC TTC CCT	342
Arg Leu Pro Gly Cys Pro Arg Gly Val Asp Pro Val Val Ser Phe Pro	
90 95 100	
GTG GCT CTC AGC TGT CGC TGT GGA CCC TGC CGC CGC AGC ACC TCT GAC	390
Val Ala Leu Ser Cys Arg Cys Gly Pro Cys Arg Arg Ser Thr Ser Asp	
105 110 115	
TGT GGG GGT CCC AAA GAC CAC CCC TTG ACC TGT GAC CAC CCC CAA GGA	438
Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp His Pro Gln Gly	
120 125 130 135	
TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA	486
Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu	
140 145 150	
TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA	534
Cys Thr Leu Gln Glu Asn Pro Phe Ser Gln Pro Gly Ala Pro Ile	
155 160 165	
CTT CAG TGC ATG GGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA	582
Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu	
170 175 180	
AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC	630
Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser	
185 190 195	
ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTC ATG GGG GGT	678
Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly	
200 205 210 215	
TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT	726
Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr	
220 225 230	

CAC AAA TCT TAAGGTACC
His Lys Ser

744

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Glu Met Leu Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15
Gly Ala Trp Ala Ser Arg Glu Pro Leu Arg Pro Trp Cys His Pro Ile
20 25 30
Asn Ala Ile Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
35 40 45
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Met Arg Val
50 55 60
Leu Gln Ala Val Leu Pro Pro Leu Pro Gln Val Val Cys Thr Tyr Arg
65 70 75 80
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
85 90 95
Asp Pro Val Val Ser Phe Pro Val Ala Leu Ser Cys Arg Cys Gly Pro
100 105 110
Cys Arg Arg Ser Thr Ser Asp Cys Gly Gly Pro Lys Asp His Pro Leu
115 120 125
Thr Cys Asp His Pro Gln Gly Ser Gly Ser Gly Ser Ala Pro
130 135 140
Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe
145 150 155 160
Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser
165 170 175
Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln
180 185 190
Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn
195 200 205
Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys
210 215 220
His Cys Ser Thr Cys Tyr Tyr His Lys Ser
225 230

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 718 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGTACCTTAA	GATTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTAA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTGGA	CCAACATCGT	CTTCTTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCA	TGCAGTGAAG	TATTGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTCCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCT	TGGGGTGGT	CACAGGTCAA	GGGGTGGTCT	TTGGGACCCC	CACAGTCAGA	360
GGTGCTGCG	CGGCAGGGTC	CACAGCGACA	GCTGAGAGCC	ACAGGGAAAGG	AGACCAACGGG	420
GTCCACGCCA	CGCGGGCAGC	CAGGGAGCCG	GATGGACTCG	AAGCGCACAT	CACGGTAGGT	480
GCACACCACC	TGAGGCAGGG	GGGGCAGGAC	CGCCTGCAGC	ACGCGCATCA	TGGTGGGGCA	540
GTAGCCGGCA	CAGATGGTGG	TGTTGACGGT	GATGCACACG	GGGCAGCCCT	CCTTCTCCAC	600
AGCCAGGATG	GCATTGATGG	GGTGGCACCA	TGGCGAAGC	GGCTCCCTGG	ATGCCCATGC	660
CCCGCCCATG	CTCAGCAGCA	GCAACAGCAG	CAGCCCCCTGG	AGCATCTCCA	TTCCCTTGG	718

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...719
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG	ATG	AAG	ACA	CTC	CAG	TTT	TTC	53					
				Met	Lys	Thr	Leu	Gln	Phe	Phe						
				1				5								
TTC	CTT	TTC	TGT	TGC	TGG	AAA	GCA	ATC	TGC	AAT	AGC	TGT	GAG	CTG	101	
Phe	Leu	Phe	Cys	Cys	Trp	Lys	Ala	Ile	Cys	Cys	Asn	Ser	Cys	Glu	Leu	
10		15													20	
ACC	AAC	ATC	ACC	ATT	GCA	ATA	GAG	AAA	GAA	GAA	TGT	CGT	TTC	TGC	ATA	149
Thr	Asn	Ile	Thr	Ile	Ala	Ile	Glu	Lys	Glu	Glu	Cys	Arg	Phe	Cys	Ile	
25					30						35					
AGC	ATC	AAC	ACC	ACT	TGG	TGT	GCT	GGC	TAC	TGC	TAC	ACC	AGG	GAT	CTG	197
Ser	Ile	Asn	Thr	Thr	Trp	Cys	Ala	Gly	Tyr	Cys	Tyr	Thr	Arg	Asp	Leu	
40					45					50					55	
GTG	TAT	AAG	GAC	CCA	GCC	AGG	CCC	AAA	ATC	CAG	AAA	ACA	TGT	ACC	TTC	245
Val	Tyr	Lys	Asp	Pro	Ala	Arg	Pro	Lys	Ile	Gln	Lys	Thr	Cys	Thr	Phe	
60									65					70		
AAG	GAA	CTG	GTA	TAT	GAA	ACA	GTG	AGA	GTG	CCC	GGC	TGT	GCT	CAC	CAT	293
Lys	Glu	Leu	Val	Tyr	Glu	Thr	Val	Arg	Val	Pro	Gly	Cys	Ala	His	His	
75					80								85			
GCA	GAT	TCC	TTG	TAT	ACA	TAC	CCA	GTG	GCC	ACC	CAG	TGT	CAC	TGT	GGC	341

Ala Asp Ser Leu Tyr Thr Tyr Pro Val Ala Thr Gln Cys His Cys Gly			
90	95	100	
AAG TGT GAC AGC GAC ACT GAT TGT ACT GTG CGA GGC CTG GGG CCC			389
Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val Arg Gly Leu Gly Pro			
105	110	115	
AGC TAC TGC TCC TTT GGT GAA ATG AAA GAA GGA TCC GGT AGC GGA TCT			437
Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu Gly Ser Gly Ser Gly Ser			
120	125	130	135
GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA TGC ACG CTA CAG GAA			485
Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu			
140	145	150	
AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA CTT CAG TGC ATG GGC			533
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly			
155	160	165	
TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA AGG TCC AAG AAG ACG			581
Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr			
170	175	180	
ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC ACT TGC TGT GTA GCT			629
Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala			
185	190	195	
AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT TTC AAA GTG GAG AAC			677
Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn			
200	205	210	215
CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT CAC AAA TCT TAAGGTACC			728
His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser			
220	225		
			728

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Lys Thr Leu Gln Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile			
1	5	10	15
Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys			
20	25	30	
Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly			
35	40	45	
Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys			

50	55	60	
Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg			
65	70	75	80
Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val			
85	90	95	
Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys			
100	105	110	
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys			
115	120	125	
Glu Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys			
130	135	140	
Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala			
145	150	155	160
Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr			
165	170	175	
Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser			
180	185	190	
Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met			
195	200	205	
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys			
210	215	220	
Tyr Tyr His Lys Ser			
225			

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGTACCTTAA GATTGTGAT AATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC	60
TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTAA GCTACACAGC AAGTGGACTC	120
TGAGGTGACG TTCTTTGGA CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC	180
TCTAGAGAAC CAGCAGCCCCA TGCACTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG	240
GTTCCTGT AGCGTGCATT CTGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT	300
ACCGGATCCT TCTTTCATTT CACCAAAGGA GCAGTAGCTG GGCCCCAGGC CTCGCACAGT	360
ACAATCAGTG CTGTCGCTGT CACACTTGGC ACAGTGACAC TGGGTGGCCA CTGGGTATGT	420
ATACAAGGAA TCTGCATGGT GAGCACAGCC GGGCACTCTC ACTGTTTCAT ATACCAGTTC	480
CTTGAAGGTA CATGTTTCT GGATTTGGG CCTGGCTGGG TCCTTATACA CCAGATCCCT	540
GGTGTAGCAG TAGCCAGCAC ACCAAGTGGT GTTGATGCTT ATGCAGAAAC GACATTCTTC	600
TTCTCTATT GCAATGGTGA TGTTGGTCAG CTCACAGCTA TTGCAGCAGA TTGCTTTCCA	660
GCAACAGAAA AGGAAGAAAA ACTGGAGTGT CTTCATCCTT GG	702

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 33...743

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG GAG ATG TTC CAG GGG CTG Met Glu Met Phe Gln Gly Leu 1 5	53
CTG CTG TTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu 10 15 20	101
CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu 25 30 35	149
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala 40 45 50 55	197
GCC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala 60 65 70	245
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile 75 80 85	293
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala 90 95 100	341
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC GAC AGC GAC AGC ACT GAT Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Asp Ser Asp Ser Thr Asp 105 110 115	389
TGT ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC TCC TTT GGT GAA ATG Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met 120 125 130 135	437
AAA GAA GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT Lys Glu Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp 140 145 150	485
TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly 155 160 165	533
GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro 170 175 180	581
ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr	629

185

190

195

TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA
 Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val
 200 205 210 215

677

ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT
 Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr
 220 225 230

725

TGT TAT TAT CAC AAA TCT TAAGGTACC
 Cys Tyr Tyr His Lys Ser
 235

752

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
 1 5 10 15
 Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
 20 25 30
 Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
 35 40 45
 Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
 50 55 60
 Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
 65 70 75 80
 Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
 85 90 95
 Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
 100 105 110
 Cys Asp Ser Asp Ser Thr Asp Cys Thr Val Arg Gly Leu Gly Pro Ser
 115 120 125
 Tyr Cys Ser Phe Gly Glu Met Lys Glu Gly Ser Gly Ser Gly Ser Gly
 130 135 140
 Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn
 145 150 155 160
 Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys
 165 170 175
 Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met
 180 185 190
 Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys
 195 200 205
 Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His
 210 215 220
 Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser

225

230

235

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTACCTTAA	GATTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTAA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTGGA	CCAACATCGT	CTTCTTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCCA	TGCACTGAAG	TATTGGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTCCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCT	TCTTCATTT	CACCAAAGGA	GCAGTAGCTG	GGCCCCAGGC	CTCGCACAGT	360
ACAATCAGTG	CTGTCGCTGT	CCGAGAGTGC	ACATTGACAG	CTGAGAGCCA	CGGCGTAGGA	420
GACCACGGGG	TTCACGCCGC	GCAGGGCAGCC	AGGGAGCCGG	ATGGACTCGA	AGCGCACATC	480
GCGGTAGTTG	CACACCACCT	GAGGCAGGGC	CGGCAGGACC	CCCTGCAGCA	CGCGGGTCAT	540
GGTGGGGCAG	TAGCCGGCAC	AGATGGTGGT	GTTGACGGTG	ATGCACACGG	GGCAGCCCTC	600
CTTCTCCACA	GCCAGGGTGG	CATTGATGGG	GCAGGCACCGT	GGCCGAAGCG	GCTCCTTGGA	660
TGCCCATGTC	CCGCCATGTC	TCAGCAGCAG	CAACAGCAGC	AGCCCCTGGA	ACATCTCCAT	720
CCTTGG						726

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...743
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG	ATG	GAG	ATG	TTC	CAG	GGG	CTG	53					
				Met	Glu	Met	Phe	Gln	Gly	Leu						
				1				5								
CTG	CTG	TTG	CTG	CTG	AGC	ATG	GGC	GGG	ACA	TGG	GCA	TCC	AAG	GAG	101	
Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly	Gly	Thr	Trp	Ala	Ser	Lys	Glu		
					10		15		20							
CCG	CTT	CGG	CCA	CGG	TGC	CGC	CCC	ATC	AAT	GCC	ACC	CTG	GCT	GTG	GAG	149
Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu	Ala	Val	Glu	
					25		30		35							
AAG	GAG	GGC	TGC	CCC	GTG	TGC	ATC	ACC	GTC	AAC	ACC	ACC	ATC	TGT	GCC	197
Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr	Ile	Cys	Ala	

40	45	50	55	
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala 60		65	70	245
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile 75	80		85	293
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala 90	95		100	341
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp 105	110		115	389
TGC ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC TCC TTT GGT GAA ATG Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met 120	125	130	135	437
AAA GAA GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT Lys Glu Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp 140	145		150	485
TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly 155	160		165	533
GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro 170	175		180	581
ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr 185	190		195	629
TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val 200	205	210	215	677
ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr 220	225		230	725
TGT TAT TAT CAC AAA TCT TAAGGTACC Cys Tyr Tyr His Lys Ser 235				752

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 237 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
20 25 30
Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
35 40 45
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
50 55 60
Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
65 70 75 80
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
85 90 95
Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
100 105 110
Cys Arg Arg Ser Thr Thr Asp Cys Thr Val Arg Gly Leu Gly Pro Ser
115 120 125
Tyr Cys Ser Phe Gly Glu Met Lys Glu Gly Ser Gly Ser Gly
130 135 140
Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn
145 150 155 160
Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys
165 170 175
Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met
180 185 190
Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys
195 200 205
Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His
210 215 220
Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
225 230 235

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 726 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTACCTTAA	GATTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTAA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTGGA	CCAACATCGT	CTTCCTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCCA	TGCACTGAAG	TATTGGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTCCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCT	TCTTCATTT	CACCAAAGGA	GCAGTAGCTG	GGCCCCAGGC	CTCGCACAGT	360
GCAGTCAGTG	GTGCTGCGGC	GGCAGAGTGC	ACATTGACAG	CTGAGAGCCA	CGGGTAGGA	420
GACCACGGGG	TTCACGCCGC	GCGGGCAGCC	AGGGAGCCGG	ATGGACTCGA	AGCGCACATC	480

GCGGTAGTTG	CACACCACCT	GAGGCAGGGC	CGGCAGGACC	CCCTGCAGCA	CGCGGGTCAT	540
GGTGGGGCAG	TAGCCGGCAC	AGATGGTGGT	GTTGACGGTG	ATGCACACGG	GGCAGCCCTC	600
CTTCTCCACA	GCCAGGGTGG	CATTGATGGG	CGGGCACCGT	GGCCGAAGCG	GCTCCTTGGA	660
TGCCCATGTC	CCGCCATGC	TCAGCAGCAG	CAACAGCAGC	AGCCCCTGGA	ACATCTCCAT	720
						726

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 743 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG	ATG	GAG	ATG	TTC	CAG	GGG	CTG	53
				Met	Glu	Met	Phe	Gln	Gly	Leu	
				1						5	
CTG	CTG	TTG	CTG	CTG	AGC	ATG	GGC	GGG	ACA	TGG	101
Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly	Gly	Thr	Trp	
10					15				20		
CCG	CTT	CGG	CCA	CGG	TGC	CGC	CCC	ATC	AAT	GCC	149
Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	
25					30				35		
AAG	GAG	GGC	TGC	CCC	GTC	TGC	ATC	ACC	AAC	ACC	197
Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	
40					45				50		
Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	245
					60				65		
										70	
CTG	CCT	CAG	GTG	GTG	TGC	AAC	TAC	CGC	GAT	GTG	293
Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	
75					80					85	
CGG	CTC	CCT	GGC	TGC	CCG	CGC	GGC	GTC	AAC	CCC	341
Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	
90					95				100		
GTG	GCT	CTC	AGC	TGT	CAA	TGT	GCA	CTC	TGC	CGC	389
Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	
105					110				115		
TGC	ACT	GTG	CGA	GGC	CTG	GGG	CCC	AGC	TAC	TCC	437
Cys	Thr	Val	Arg	Gly	Leu	Gly	Pro	Ser	Tyr	Cys	
120					125				130		
										135	

TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA Ser Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu 140 145 150	485
TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile 155 160 165	533
CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu 170 175 180	581
AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser 185 190 195	629
ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTC ATA ATG GGG GGT Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly 200 205 210 215	677
TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr 220 225 230	725
CAC AAA TCT TAAGGTACC His Lys Ser	743

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly 1 5 10 15
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile 20 25 30
Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr 35 40 45
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val 50 55 60
Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg 65 70 75 80
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val 85 90 95
Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu 100 105 110

Cys Arg Arg Ser Thr Thr Asp Cys Thr Val Arg Gly Leu Gly Pro Ser
 115 120 125
 Tyr Cys Ser Phe Gly Glu Gly Ser Gly Ser Gly Ser Ala Pro
 130 135 140
 Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe
 145 150 155 160
 Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser
 165 170 175
 Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln
 180 185 190
 Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn
 195 200 205
 Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys
 210 215 220
 His Cys Ser Thr Cys Tyr Tyr His Lys Ser
 225 230

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 717 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTACCTTAA	GATTGTGAT	ATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTTGAAACCC	CCCATTAATCG	TGACCCTGTT	ATATGATTAA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTGGAA	CCAACATCGT	CTTCTTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCCA	TGCACTGAAG	TATTGGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTCCTCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCT	TCACCAAAGG	AGCAGTAGCT	GGGCCCCAGG	CCTCGCACAG	TGCAGTCAGT	360
GGTGCTGCGG	CGGCAGAGTG	CACATTGACA	GCTGAGAGCC	ACGGCGTAGG	AGACCACGGG	420
GTTCACGCCG	CGCGGGCAGC	CAGGGAGCCG	GATGGACTCG	AAGCGCACAT	CGCGGTAGTT	480
GCACACCACC	TGAGGCAGGG	CCGGCAGGAC	CCCCTGCAGC	ACGCGGGTCA	TGGTGGGGCA	540
GTAGCCGGCA	CAGATGGTGG	TGTTGACGGT	GATGCCACACG	GGGCAGCCCT	CCTTCTCCAC	600
AGCCAGGGTG	GCATTGATGG	GGCGGCACCG	TGGCCGAAGC	GGCTCCTTGG	ATGCCCATGT	660
CCCGCCCCATG	CTCAGCAGCA	GCAACAGCAG	CAGCCCCCTGG	AACATCTCCA	TCCTTGG	717

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 743 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...734
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATGAAATCGA CGGAATCAGA CTCGAGCAA GG ATG GAG ATG TTC CAG GGG CTG Met Glu Met Phe Gln Gly Leu	1	5	53
CTG CTG TTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu	10	15	101
CCG CTT CGG CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu	25	30	149
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala	40	45	197
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala	60	65	245
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile	75	80	293
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala	90	95	341
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp	105	110	389
TGC ACT GTG CGA GGC CTG GGG CCC AGC TAC TGC GAT GAC CCG CGG GGA Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Asp Asp Pro Arg Gly	120	125	437
TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu	140	145	485
TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile	155	160	533
CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu	170	175	581
AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC ACC TCA GAG TCC Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser	185	190	629
ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly	200	205	677
TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT			725

Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr
220 225 230

CAC AAA TCT TAAGGTACC
His Lys Ser

743

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
20 25 30
Asn Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
35 40 45
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
50 55 60
Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
65 70 75 80
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
85 90 95
Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
100 105 110
Cys Arg Arg Ser Thr Thr Asp Cys Thr Val Arg Gly Leu Gly Pro Ser
115 120 125
Tyr Cys Asp Asp Pro Arg Gly Ser Gly Ser Gly Ser Ala Pro
130 135 140
Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe
145 150 155 160
Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser
165 170 175
Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln
180 185 190
Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn
195 200 205
Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys
210 215 220
His Cys Ser Thr Cys Tyr His Lys Ser
225 230

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 717 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTACCTTAA	GATTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTAA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTGGA	CCAACATCGT	CTTCTTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCCA	TGCACTGAAG	TATTGGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTCCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCC	CGCGGGTCAT	CGCAGTAGCT	GGGCCCCAGG	CCTCGCACAG	TGCAGTCAGT	360
GGTGCTGCGG	CGGCAGAGTG	CACATTGACA	GCTGAGAGCC	ACGGCGTAGG	AGACCACGGG	420
GTTCACGCCG	CGCGGGCAGC	CAGGGAGCCG	GATGGACTCG	AAGCGCACAT	CGCGGTAGTT	480
GCACACCACC	TGAGGCAGGG	CCGGCAGGAC	CCCCTGCAGC	ACGCGGGTCA	TGGTGGGGCA	540
GTAGCCGGCA	CAGATGGTGG	TGTTGACGGT	GATGCACACG	GGGCAGCCCT	CCTTCTCCAC	600
AGCCAGGGTG	GCATTGATGG	GGCGGCACCG	TGGCCGAAGC	GGCTCCTTGG	ATGCCCATGT	660
CCCGCCCATG	CTCAGCAGCA	GCAACAGCAG	CAGCCCCTGG	AACATCTCCA	TCCTTGG	717

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...700
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG ATG AAG ACA CTC CAG	TTT TTC	53
			Met Lys Thr Leu Gln Phe Phe		
			1	5	
TTC CTT	TTC TGT	TGC TGG	AAA GCA ATC TGC TGC	AAT AGC TGT GAG CTG	101
Phe	Leu	Phe	Cys Cys Trp Lys Ala Ile	Cys Cys Asn Ser Cys Glu Leu	
10	15		15	20	
ACC AAC ATC ACC ATT GCA ATA GAG AAA GAA GAA TGT CGT	TTC TGC ATA	149			
Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg	Phe Cys Ile				
25	30	35			
AGC ATC AAC ACC ACT TGG TGT GCT GGC TAC TGC TAC ACC AGG	GAT CTG	197			
Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp	Leu				
40	45	50	55		
GTG TAT AAG GAC CCA GCC AGG CCC AAA ATC CAG AAA ACA TGT ACC	TTC	245			
Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe					
60	65	70			
AAG GAA CTG GTA TAT GAA ACA GTG AGA GTG CCC GGC TGT GCT CAC CAT	293				
Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His					

75	80	85	
GCA GAT TCC TTG TAT ACA TAC CCA GTG GCC ACC CAG TGT CAC TGT GGC Ala Asp Ser Leu Tyr Thr Tyr Pro Val Ala Thr Gln Cys His Cys Gly 90 95 100			341
AAG TGT GAC AGC GAC AGC ACT GAT TGT ACT GTG CGA GGC CTG GGG CCC Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val Arg Gly Leu Gly Pro 105 110 115			389
AGC TAC TGC TCC TTT GGT GAA GGA TCC GGT AGC GGA TCT GGT AGC GCT Ser Tyr Cys Ser Phe Gly Glu Gly Ser Gly Ser Gly Ser Ala 120 125 130 135			437
CCT GAT GTG CAG GAT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe 140 145 150			485
TTC TCC CAG CCG GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe 155 160 165			533
TCT AGA GCA TAT CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val 170 175 180			581
CAA AAG AAC GTC ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr 185 190 195			629
AAC AGG GTC ACA GTA ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala 200 205 210 215			677
TGC CAC TGC AGT ACT TGT TAT TA TCACAAATCT TAAGGTACC Cys His Cys Ser Thr Cys Tyr Tyr 220			719

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Lys Thr Leu Gln Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile 1 5 10 15	
Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys 20 25 30	
Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly	

84

35	40	45	
Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys			
50	55	60	
Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg			
65	70	75	80
Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val			
85	90	95	
Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys			
100	105	110	
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Gly Ser			
115	120	125	
Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys			
130	135	140	
Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu			
145	150	155	160
Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg			
165	170	175	
Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr			
180	185	190	
Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe			
195	200	205	
Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr			
210	215	220	

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 693 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGTACCTTAA GATTGTGAT ATAACAAGT ACTGCAGTGG CACGCCGTGT GGTTCTCCAC	60
TTTGAAACCC CCCATTACTG TGACCCTGTT ATATGATTAA GCTACACAGC AAGTGGACTC	120
TGAGGTGACG TTCTTTGGA CCAACATCGT CTTCTTGGAC CTTAGTGGAG TGGGATATGC	180
TCTAGAGAAC CAGCAGCCCA TGCAGTGAAG TATTGGGGCA CCCGGCTGGG AGAAGAATGG	240
GTTCCTGT AGCGTGCATT CTGGCAATC CTGCACATCA GGAGCGCTAC CAGATCCGCT	300
ACCGGATCCT TCACCAAAGG AGCAGTAGCT GGGCCCCAGG CCTCGCACAG TACAATCAGT	360
GCTGTCGCTG TCACACTTGC CACAGTGACA CTGGGTGGCC ACTGGGTATG TATACAAGGA	420
ATCTGCATGG TGAGCACAGC CGGGCACTCT CACTGTTCA TATACCAGTT CCTTGAAGGT	480
ACATGTTTC TGGATTTGG GCCTGGCTGG GTCCTTATAC ACCAGATCCC TGGTAGCA	540
GTAGCCAGCA CACCAAGTGG TGTTGATGCT TATGCAGAAA CGACATTCTT CTTCTCTAT	600
TGCAATGGTG ATGTTGGTCA GCTCACAGCT ATTGCAGCAG ATTGCTTCC AGCAACAGAA	660
AAGGAAGAAA AACTGGAGTG TCTTCATCCT TGG	693

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 707 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 33...698

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG ATG AAG ACA CTC CAG TTT TTC Met Lys Thr Leu Gln Phe Phe 1 5	53
TTC CTT TTC TGT TGC TGG AAA GCA ATC TGC TGC AAT AGC TGT GAG CTG Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys Asn Ser Cys Glu Leu 10 15 20	101
ACC AAC ATC ACC ATT GCA ATA GAG AAA GAA GAA TGT CGT TTC TGC ATA Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe Cys Ile 25 30 35	149
AGC ATC AAC ACC ACT TGG TGT GCT GGC TAC TGC TAC ACC AGG GAT CTG Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu 40 45 50 55	197
GTG TAT AAG GAC CCA GCC AGG CCC AAA ATC CAG AAA ACA TGT ACC TTC Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe 60 65 70	245
AAG GAA CTG GTA TAT GAA ACA GTG AGA GTG CCC GGC TGT GCT CAC CAT Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His 75 80 85	293
GCA GAT TCC TTG TAT ACA TAC CCA GTG GCC ACC CAG TGT CAC TGT GGC Ala Asp Ser Leu Tyr Thr Pro Val Ala Thr Gln Cys His Cys Gly 90 95 100	341
AAG TGT GAC AGC GAC AGC ACT GAT TGT ACT GTG CGA GGC CTG GGG CCC Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val Arg Gly Leu Gly Pro 105 110 115	389
AGC TAC TGC GGA TCC GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG Ser Tyr Cys Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln 120 125 130 135	437
GAT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro 140 145 150	485
GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr 155 160 165	533
CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val 170 175 180	581
ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr	629

185

190

195

GTA ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT
 Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser
 200 205 210 215

677

ACT TGT TAT TAT CAC AAA TCT TAAGGTACC
 Thr Cys Tyr Tyr His Lys Ser
 220

707

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Lys Thr Leu Gln Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
 1 5 10 15
 Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
 20 25 30
 Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
 35 40 45
 Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
 50 55 60
 Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
 65 70 75 80
 Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
 85 90 95
 Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
 100 105 110
 Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Gly Ser Gly Ser Gly Ser
 115 120 125
 Gly Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
 130 135 140
 Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly
 145 150 155 160
 Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr
 165 170 175
 Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala
 180 185 190
 Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn
 195 200 205
 His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
 210 215 220

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGTACCTTAA	GATTGTGAT	AATAACAAGT	ACTGCAGTGG	CACGCCGTGT	GGTTCTCCAC	60
TTGAAACCC	CCCATTACTG	TGACCCTGTT	ATATGATTAA	GCTACACAGC	AAGTGGACTC	120
TGAGGTGACG	TTCTTTGGA	CCAACATCGT	CTTCTTGGAC	CTTAGTGGAG	TGGGATATGC	180
TCTAGAGAAG	CAGCAGCCCA	TGCAGTGAAG	TATTGGGCA	CCCGGCTGGG	AGAAGAATGG	240
GTTCCTGT	AGCGTGCATT	CTGGGCAATC	CTGCACATCA	GGAGCGCTAC	CAGATCCGCT	300
ACCGGATCCG	CAGTAGCTGG	GCCCCAGGCC	TCGCACAGTA	CAATCAGTGC	TGTCGCTGTC	360
ACACTTGCCA	CAGTGACACT	GGGTGGCAC	TGGGTATGTA	TACAAGGAAT	CTGCATGGTG	420
AGCACAGCCG	GGCACTCTCA	CTGTTTCATA	TACCAGTTCC	TTGAAGGTAC	ATGTTTCTG	480
GATTTGGGC	CTGGCTGGGT	CCTTATACAC	CAGATCCCTG	GTGTAGCAGT	AGCCAGCACA	540
CCAAGTGGTG	TTGATGCTTA	TGCAGAAACG	ACATCTTCT	TTCTCTATTG	CAATGGTGAT	600
GTGGTCAGC	TCACAGCTAT	TGCAGCAGAT	TGCTTCCAG	CAACAGAAAA	GGAAGAAAAA	660
CTGGAGTGTC	TTCATCCTTG	G				681

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 312 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...303
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGC	GGA	TCC	GGT	AGC	GGA	TCT	GGT	AGC	GCT	CCT	GAT	GTG	CAG	GAT	TGC	48
Cys	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Ala	Pro	Asp	Val	Gln	Asp	Cys	
1			5				10						15			
CCA	GAA	TGC	ACG	CTA	CAG	GAA	AAC	CCA	TTC	TTC	TCC	CAG	CCG	GGT	GCC	96
Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe	Ser	Gln	Pro	Gly	Ala	
			20				25					30				
CCA	ATA	CTT	CAG	TGC	ATG	GGC	TGC	TGC	TTC	TCT	AGA	GCA	TAT	CCC	ACT	144
Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr	
			35				40				45					
CCA	CTA	AGG	TCC	AAG	AAG	ACG	ATG	TTG	GTC	CAA	AAG	CAA	GTC	ACC	TCA	192
Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Gln	Lys	Gln	Val	Thr	Ser	
			50				55			60						
GAG	TCC	ACT	TGC	TGT	GTA	GCT	AAA	TCA	TAT	AAC	AGG	GTC	ACA	GTA	ATG	240
Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr	Asn	Arg	Val	Thr	Val	Met	
			65				70			75		80				
GGG	GGT	TTC	AAA	GTG	GAG	CAA	CAC	ACG	GCG	TGC	CAC	TGC	AGT	ACT	TGT	288

Gly Gly Phe Lys Val Glu Gln His Thr Ala Cys His Cys Ser Thr Cys
85 90 95

TAT TAT CAC AAA TCT TAAGGTACC
Tyr Tyr His Lys Ser
100

312

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (iii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Cys Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys
1 5 10 15
Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala
20 25 30
Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr
35 40 45
Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Gln Val Thr Ser
50 55 60
Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
65 70 75 80
Gly Gly Phe Lys Val Glu Gln His Thr Ala Cys His Cys Ser Thr Cys
85 90 95
Tyr Tyr His Lys Ser
100

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTACCGGTAC CTTAAGATTT GTGATAATAA CAAGTACTGC AGTGGCACGC CGTGTGTTGC 60
TCCACTTTGA AACCCCCCAT TACTGTGACC CTGTTATATG ATTTAGCTAC ACAGCAAGTG 120
GACTCTGAGG TGACTTGCTT TTGGACCAAC ATCGTCTTCT TGGACCTTAG TGGAGTGGGA 180
TATGCTCTAG AGAACGAGCA GCCCATGCAC TGAAGTATTG GGGCACCCGG CTGGGAGAAG 240
AATGGGTTTT CCTGTAGCGT GCATTCTGGG CAATCCTGCA CATCAGGAGC GCTACCAGAT 300
CCGCTACCGG ATCCGCA 317

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 33...575
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATGAAATCGA CGGAATCAGA CTCGAGCAA GG ATG GAG ATG TTC CAG GGG CTG Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu	53
1 5	
CTG CTG TTG CTG CTG AGC ATG GGC GGG ACA TGG GCA TCC AAG GAG Leu Leu Leu Leu Leu Ser Met Gly Gly Thr Trp Ala Ser Lys Glu	101
10 15 20	
CCG CTT CGG CCA CGG TGC CGC CCC ATC CAA GCC ACC CTG GCT GTG GAG Pro Leu Arg Pro Arg Cys Arg Pro Ile Gln Ala Thr Leu Ala Val Glu	149
25 30 35	
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala	197
40 45 50 55	
GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala	245
60 65 70	
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile	293
75 80 85	
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala	341
90 95 100	
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp	389
105 110 115	
TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe	437
120 125 130 135	
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC AGC CTT CCA AGC CCA Gln Asp Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro	485
140 145 150	
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln Gly Ser	533
155 160 165	

GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA
Gly Ser Gly Ser Gly Ser Ala Pro Asp Val Gln Asp Cys Pro
170 175 180

575

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile
20 25 30
Gln Ala Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr
35 40 45
Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val
50 55 60
Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg
65 70 75 80
Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val
85 90 95
Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu
100 105 110
Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu
115 120 125
Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Lys Ala Pro
130 135 140
Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr
145 150 155 160
Pro Ile Leu Pro Gln Gly Ser Gly Ser Gly Ser Ala Pro Asp
165 170 175
Val Gln Asp Cys Pro
180

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TGGGCAATCC TGCACATCAG GAGCGCTACC AGATCCGCTA CCGGATCCTT GGGGGAGGAT
CGGGGTGTCC GAGGGCCCCG GGAGTCGGGA TGGGCTTGGGA AGGCTGGGGG GAGGGGCCTT
TGAGGAAGAG GAGTCCTGGGA AGCGGGGGTC ATCACAGGTC AAGGGGTGGT CCTTGGGACC

60

120

180

CCCGCAGTCA	GTGGTGCTGC	GGCGGCAGAG	TGCACATTGA	CAGCTGAGAG	CCACGGCGTA	240
GGAGACCACG	GGGTTCACGC	CGCGCGGGCA	GCCAGGGAGC	CGGATGGACT	CGAAGCGCAC	300
ATCGCGGTAG	TTGCACACCA	CCTGAGGCAG	GGCCGGCAGG	ACCCCCTGCA	GCACGCGGGT	360
CATGGTGGGG	CAGTAGCCGG	CACAGATGGT	GGTGTGACG	GTGATGCACA	CGGGGCAGCC	420
CTCCTTCTCC	ACAGCCAGGG	TGGCTTGGAT	GGGGCGGCAC	CGTGGCCGAA	GCGGCTCCTT	480
GGATGCCCAT	GTCCCCCCA	TGCTCAGCAG	CAGCAAACAGC	AGCAGCCCC	GGAACATCTC	540
CATCCTTGG						549

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 33...827

- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATGAAATCGA	CGGAATCAGA	CTCGAGCCAA	GG	ATG	GAG	ATG	TTC	CAG	GGG	CTG	53					
				Met	Glu	Met	Phe	Gln	Gly	Leu						
				1				5								
CTG	CTG	CTG	CTG	CTG	AGC	ATG	GGC	GGG	ACA	TGG	GCA	TCC	AAG	GAG	101	
Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly	Gly	Thr	Trp	Ala	Ser	Lys	Glu		
10					15				20							
CCG	CTT	CGG	CCA	CGG	TGC	CGC	CCC	ATC	AAT	GCC	ACC	CTG	GCT	GTG	GAG	149
Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu	Ala	Val	Glu	
25					30				35							
AAG	GAG	GGC	TGC	CCC	GTG	TGC	ATC	ACC	GTC	AAC	ACC	ACC	ATC	TGT	GCC	197
Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr	Ile	Cys	Ala	
40					45				50			55				
GGC	TAC	TGC	CCC	ACC	ATG	ACC	CGC	GTG	CTG	CAG	GGG	GTC	CTG	CCG	GCC	245
Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val	Leu	Pro	Ala	
60					65					70						
CTG	CCT	CAG	GTG	GTG	TGC	AAC	TAC	CGC	GAT	GTG	CGC	TTC	GAG	TCC	ATC	293
Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe	Glu	Ser	Ile	
75					80					85						
CGG	CTC	CCT	GGC	TGC	CCG	CGC	GGC	GTG	AAC	CCC	GTG	GTC	TCC	TAC	GCC	341
Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val	Ser	Tyr	Ala	
90					95				100							
GTG	GCT	CTC	AGC	TGT	CAA	TGT	GCA	CTC	TGC	CGC	CGC	AGC	ACC	ACT	GAC	389
Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	Arg	Ser	Thr	Thr	Asp	
105					110				115							
TGC	GGG	GGT	CCC	AAG	GAC	CAC	CCC	TTG	ACC	TGT	GAT	GAC	CCC	CGC	TTC	437

Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys	Asp	Asp	Pro	Arg	Phe	
120										130						135
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA															485	
Gln	Asp	Ser	Ser	Ser	Ser	Lys	Ala	Pro	Pro	Pro	Ser	Leu	Pro	Ser	Pro	
																140 145 150
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCC CAA GGA TCC															533	
Ser	Arg	Leu	Pro	Gly	Pro	Ser	Asp	Thr	Pro	Ile	Leu	Pro	Gln	Gly	Ser	
																155 160 165
GGT AGC GGA TCT GGT AGC GCT CCT GAT GTG CAG GAT TGC CCA GAA TGC															581	
Gly	Ser	Gly	Ser	Gly	Ser	Ala	Pro	Asp	Val	Gln	Asp	Cys	Pro	Glu	Cys	
																170 175 180
ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG GGT GCC CCA ATA CTT															629	
Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe	Ser	Gln	Pro	Gly	Ala	Pro	Ile	Leu	
																185 190 195
CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT CCC ACT CCA CTA AGG															677	
Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg	Ala	Tyr	Pro	Thr	Pro	Leu	Arg	
																200 205 210 215
TCC AAG AAG ACG ATG TTG GTC CAA AAG CAA GTC ACC TCA GAG TCC ACT															725	
Ser	Lys	Lys	Thr	Met	Leu	Val	Gln	Lys	Gln	Val	Thr	Ser	Glu	Ser	Thr	
																220 225 230
TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA GTA ATG GGG GGT TTC															773	
Cys	Cys	Val	Ala	Lys	Ser	Tyr	Asn	Arg	Val	Thr	Val	Met	Gly	Gly	Phe	
																235 240 245
AAA GTG GAG CAA CAC ACG GCG TGC CAC TGC AGT ACT TGT TAT TAT CAC															821	
Lys	Val	Glu	Gln	His	Thr	Ala	Cys	His	Cys	Ser	Thr	Cys	Tyr	Tyr	His	
																250 255 260
AAA TCT TAAGTTAAC															837	
Lys	Ser															265

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Glu	Met	Phe	Gln	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Ser	Met	Gly	
1				5					10				15		
Gly Thr Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile															
									20	25			30		

Asn	Ala	Thr	Leu	Ala	Val	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr		
35						40					45				
Val	Asn	Thr	Thr	Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val
50						55					60				
Leu	Gln	Gly	Val	Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg
65						70				75				80	
Asp	Val	Arg	Phe	Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val
						85				90			95		
Asn	Pro	Val	Val	Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu
						100				105			110		
Cys	Arg	Arg	Ser	Thr	Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu
						115				120			125		
Thr	Cys	Asp	Asp	Pro	Arg	Phe	Gln	Asp	Ser	Ser	Ser	Lys	Ala	Pro	
						130				135			140		
Pro	Pro	Ser	Leu	Pro	Ser	Pro	Ser	Arg	Leu	Pro	Gly	Pro	Ser	Asp	Thr
145						150				155			160		
Pro	Ile	Leu	Pro	Gln	Gly	Ser	Gly	Ser	Gly	Ser	Ala	Pro	Asp		
						165				170			175		
Val	Gln	Asp	Cys	Pro	Glu	Cys	Thr	Leu	Gln	Glu	Asn	Pro	Phe	Phe	Ser
						180				185			190		
Gln	Pro	Gly	Ala	Pro	Ile	Leu	Gln	Cys	Met	Gly	Cys	Cys	Phe	Ser	Arg
						195				200			205		
Ala	Tyr	Pro	Thr	Pro	Leu	Arg	Ser	Lys	Lys	Thr	Met	Leu	Val	Gln	Lys
						210				215			220		
Gln	Val	Thr	Ser	Glu	Ser	Thr	Cys	Cys	Val	Ala	Lys	Ser	Tyr	Asn	Arg
225						230				235			240		
Val	Thr	Val	Met	Gly	Gly	Phe	Lys	Val	Glu	Gln	His	Thr	Ala	Cys	His
						245				250			255		
Cys	Ser	Thr	Cys	Tyr	Tyr	His	Lys	Ser							
						260				265					

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 835 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TCCGGATTAG	CTTGAGATGG	ATCCGGTTAA	CTTAAGATTG	GTGATAATAA	CAAGTACTGC	60
AGTGGCACGC	CGTGTGTTGC	TCCACTTTGA	AACCCCCCAT	TACTGTGACC	CTGTTATATG	120
ATTTAGCTAC	ACAGCAAGTG	GACTCTGAGG	TGACTTGCTT	TTGGACCAAAC	ATCGTCTTCT	180
TGGACCTTAG	TGGAGTGGGA	TATGCTCTAG	AGAACGAGCA	GCCCCATGCAC	TGAAGTATTG	240
GGGCACCCGG	CTGGGAGAAG	ATATGGTTTT	CCTGTAGCGT	GCATTCTGGG	CAATCCTGCA	300
CATCAGGAGC	GCTACCAAGAT	CCGCTACCGG	ATCCTTGGGG	GAGGATCAGGG	GTGTCCGAGG	360
GCCCCGGGAG	TCGGGATGGG	CTTGGGAAGGC	TGGGGGGAGG	GGCCTTGAG	GAAGAGGAGT	420
CCTGGAAGCG	GGGGTCATCA	CAGGTCAAGG	GGTGGTCCTT	GGGACCCCG	CAGTCAGTGG	480
TGCTGCGGGCG	GCAGAGTGCA	CATTGACAGC	TGAGAGCCAC	GGCGTAGGAG	ACCAACGGGGT	540
TCACGCCGCG	CGGGCAGCCA	GGGAGCCGGA	TGGACTCGAA	GCGCACATCG	CGGTAGTTGC	600
ACACCACCTG	AGGCAGGGCC	GGCAGGACCC	CCTGCAGCAC	GCGGGTCATG	GTGGGGCAGT	660
AGCCGGCACA	GATGGTGGTG	TTGACGGTGA	TGCACACGGG	GCAGCCCTCC	TTCTCCACAG	720
CCAGGGTGGC	ATTGATGGGG	CGGCACCGTG	GCCGAAGCGG	CTCCTTGGAT	GCCCATGTCC	780
CGCCCATGCT	CAGCAGCAGC	AACAGCAGCA	GCCCCCTGGAA	CATCTCCATC	CTTGG	835

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGAGGAAGGG TGGTCGACCT CTCTGGT

27

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACATCAGGA GCTTGTGGGA GGATCGG

27

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATCCTCCAC AAGCTCCTGA TGTGCAG

27

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TGAGTCGACA TGATAATTCA GTGATTGAAT

30

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATGAAATCGA CGGAATCAGA CTCGAGCAA GGATGGAGAT GTTCCAGGGG CTGCT

55

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCTACCAGAT CCGCTACCGG ATCCTTGGGG GAGGATCGGG GTGTCCGAGG G

51

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGATCCGGTA GCGGATCTGG TAGCGCTCCT GATGTGCAGG ATTGCCCA

48

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCCGGATTAG CTTGAGATGG ATCCGGTACC TTAAGATTTG TGATAATAAC AAGTACTGCA

60

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

ATGAAATCGA CGGAATCAGA CTCGAGCCAA GG

32

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TCCGGATTAG CTTGAGATGG ATCCGGTACC TTA

33

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15
Gly Thr Trp Ala
20

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCTACCGGAT CCCCGCGGGT CATCACAGGT CAAGGGGTGG T

41

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGAAATCGA CGGAATCAGA CTCGAGCAA GGAATGGAGA TGCTCCAGGG GCTGCT

56

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCTACCAGAT CCGCTACCGG ATCCTTGGGG GTGGTCACAG GTCAAGGGT G

51

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Glu Met Leu Gln Gly Leu Leu Leu Leu Leu Ser Met Gly
1 5 10 15
Gly Ala Trp Ala
20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATGAAATCGA CGGAATCAGA CTCGAGCAA GGATGAAGAC ACTCCAGTTT TTCTTCC

57

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACCAGATCCG CTACCGGATC CTTCTTCAT TTCACCAAAG GAGCAG

46

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15
Cys Cys

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GCTACCGGAT CCTTCTTCAT TTTCACCAAA GGAGCAGTAG CTGGGCCCA GGCCTCGCAC
AGTACAATCA GTGCTGTCGC TGTCGAGAG TGCACATTGA CAGCTGACAG C

60

111

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GCTACCGGAT CCTTCTTCAT TTTCACCAAA GGAGCAGTAG CTGGGCCCA GGCCTCGCAC
AGTGCAGTCA GTGGTGCTGC GGCAGCA

60

87

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCTACCGGAT CCTTCACCAA AGGAGCAGTA GCTGGGCCCC AGGCCTCGCA CAGTGCAGTC	60
AGTGGTGCTG CGGC GGCA	78

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCTACCGGAT CCCCGCGGGT CATCGCAGTA GCTGGGCCCC AGGCCTCGCA CAGTGCAGTC	60
AGTGGTGCTG CGGC GGCA	78

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TGCTTCTCTA GAGCATATCC CACTCCACTA AGGTCCAAGA AGACGATGTT GGTCCAAAAG	60
CAAGTCACCT	70

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTACCGGTAC CTTAAGATT GTGATAATAA CAAGTACTGC AGTGGCACGC CGTGTGTTGC	60
TCCACTTTGA AAC	73

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CGGGGTAGGT TCGGTGGGAC CGACACCTCT TCCTCCCGAC GGGG

44

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTACCACCAAC AACTGCCACT ACGTGTGCCCG CGTCGGGAGG AAGAGGTG

48

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu
1		5						10						15	
Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr
		20						25						30	
Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val
	35							40					45		
Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe
	50							55					60		
Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val
	65							70					75		80
Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	Arg	Ser
								85					90		95
Thr	Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys	Asp	Asp
								100					105		110
Pro	Arg	Phe	Gln	Asp	Ser	Ser	Ser	Ser	Lys	Ala	Pro	Pro	Pro	Ser	Leu
													115		125
Pro	Ser	Pro	Ser	Arg	Leu	Pro	Gly	Pro	Ser	Asp	Thr	Pro	Ile	Leu	Pro
								130					135		140
Gln															
145															

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu
1		5				10						15			
Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr
		20					25					30			
Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val
	35					40					45				
Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe
	50					55				60					
Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val
	65					70				75			80		
Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys	Arg	Arg	Ser
		85					90				95				
Thr	Thr	Asp	Cys	Gly	Gly	Pro	Lys	Asp	His	Pro	Leu	Thr	Cys	Asp	Asp
			100				105				110				
Pro	Arg														

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ser	Lys	Glu	Pro	Leu	Arg	Pro	Arg	Cys	Arg	Pro	Ile	Asn	Ala	Thr	Leu
1		5				10						15			
Ala	Val	Glu	Lys	Glu	Gly	Cys	Pro	Val	Cys	Ile	Thr	Val	Asn	Thr	Thr
		20					25					30			
Ile	Cys	Ala	Gly	Tyr	Cys	Pro	Thr	Met	Thr	Arg	Val	Leu	Gln	Gly	Val
	35					40					45				
Leu	Pro	Ala	Leu	Pro	Gln	Val	Val	Cys	Asn	Tyr	Arg	Asp	Val	Arg	Phe
	50					55				60					
Glu	Ser	Ile	Arg	Leu	Pro	Gly	Cys	Pro	Arg	Gly	Val	Asn	Pro	Val	Val
	65					70				75			80		
Ser	Tyr	Ala	Val	Ala	Leu	Ser	Cys	Gln	Cys	Ala	Leu	Cys			
			85				90								

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ser Arg Glu Pro Leu Arg Pro Trp Cys His Pro Ile Asn Ala Ile Leu
1 5 10 15
Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr
20 25 30
Ile Cys Ala Gly Tyr Cys Pro Thr Met Met Arg Val Leu Gln Ala Val
35 40 45
Leu Pro Pro Leu Pro Gln Val Val Cys Thr Tyr Arg Asp Val Arg Phe
50 55 60
Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val Asp Pro Val Val
65 70 75 80
Ser Phe Pro Val Ala Leu Ser Cys Arg Cys Gly Pro Cys Arg Arg Ser
85 90 95
Thr Ser Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp His
100 105 110
Pro Gln

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Val Glu Lys Glu Gly
1 5 10 15
Cys Gly Phe Cys Ile Thr Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys
20 25 30
Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln
35 40 45
Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro
50 55 60
Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val Ala Thr
65 70 75 80
Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val
85 90 95
Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu
100 105 110

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Val Glu Lys Glu Gly
1 5 10 15
Cys Gly Phe Cys Ile Thr Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys
20 25 30
Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln
35 40 45
Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro
50 55 60
Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val Ala Thr
65 70 75 80
Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val
85 90 95
Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu
100 105

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Val Glu Lys Glu Gly
1 5 10 15
Cys Gly Phe Cys Ile Thr Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys
20 25 30
Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln
35 40 45
Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg Val Pro
50 55 60
Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val Ala Thr
65 70 75 80
Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys Thr Val
85 90 95
Arg Gly Leu Gly Pro Ser Tyr Cys
100

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asp Ser Asp Ser Thr Asp Cys Thr Val Arg Gly Leu Gly Pro Ser Tyr
1 5 10 15

Cys Ser Phe Gly Glu Met Lys Glu
20

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys
1 5 10 15
Glu

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Thr Val Arg Gly Leu Gly Pro Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro
1 5 10 15
Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys
20 25 30
Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu
35 40 45
Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser
50 55 60
Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr
65 70 75 80
Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
85 90

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gly Ser Gly Ser
1

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Ser Gly Ser Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Asp Asp Pro Arg
1
